



OIPF

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RAW SEQUENCE LISTING

DATE: 08/12/2002

PATENT APPLICATION: US/10/046,060A

TIME: 14:13:18

Input Set : A:\2976-C SeqListce filed 101801.txt

Output Set: N:\CRF3\08122002\J046060A.raw

3 <110> APPLICANT: Sims, John E.
 5 <120> TITLE OF INVENTION: FIL-1 THETA DNAs AND POLYPEPTIDES
 7 <130> FILE REFERENCE: 2976-C
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/046,060A
 C--> 10 <141> CURRENT FILING DATE: 2002-07-23
 12 <150> PRIOR APPLICATION NUMBER: US 60/178,389
 13 <151> PRIOR FILING DATE: 2000-01-27
 15 <150> PRIOR APPLICATION NUMBER: US 60/195,962
 16 <151> PRIOR FILING DATE: 2000-04-11
 18 <150> PRIOR APPLICATION NUMBER: US 09/769,878
 19 <151> PRIOR FILING DATE: 2001-01-25
 21 <160> NUMBER OF SEQ ID NOS: 21
 23 <170> SOFTWARE: PatentIn version 3.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 339
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Homo sapiens
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 33 atccagggag ggagccgctg cctggcatgt gtggagacag aagaggggcc ttccctacag 120
 35 ctggaggatg tgaacattga ggaactgtac aaaggtggtg aagaggccac acgcttcacc 180
 37 ttcttcacaga gcagctcagg ctccgccttc aggttgagg ctgctgctg gcctggctgg 240
 39 ttctgtgtg gccggcaga gccccagcag ccagtacagc tcaccaagga gaggagccc 300
 41 tcagcccgtta ccaagtttta ctttgaacag agctggtag 339
 44 <210> SEQ ID NO: 2
 45 <211> LENGTH: 112
 46 <212> TYPE: PRT
 47 <213> ORGANISM: Homo sapiens
 49 <400> SEQUENCE: 2
 51 Lys Ile Cys Ile Leu Pro Asn Arg Gly Leu Ala Arg Thr Lys Val Pro
 52 1 5 10 15
 55 Ile Phe Leu Gly Ile Gln Gly Gly Ser Arg Cys Leu Ala Cys Val Glu
 56 20 25 30
 59 Thr Glu Glu Gly Pro Ser Leu Gln Leu Glu Asp Val Asn Ile Glu Glu
 60 35 40 45
 63 Leu Tyr Lys Gly Gly Glu Glu Ala Thr Arg Phe Thr Phe Phe Gln Ser
 64 50 55 60
 67 Ser Ser Gly Ser Ala Phe Arg Leu Glu Ala Ala Ala Trp Pro Gly Trp
 68 65 70 75 80
 71 Phe Leu Cys Gly Pro Ala Glu Pro Gln Gln Pro Val Gln Leu Thr Lys
 72 85 90 95
 75 Glu Ser Glu Pro Ser Ala Arg Thr Lys Phe Tyr Phe Glu Gln Ser Trp
 76 100 105 110

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79 <210> SEQ ID NO: 3
80 <211> LENGTH: 459
81 <212> TYPE: DNA
82 <213> ORGANISM: Homo sapiens
84 <220> FEATURE:
85 <221> NAME/KEY: CDS
86 <222> LOCATION: (1)..(456)
87 <223> OTHER INFORMATION:
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92 Met Cys Ser Leu Pro Met Ala Arg Tyr Tyr Ile Ile Lys Tyr Ala Asp
93 1          5          10          15
95 cag aag gct cta tac aca aga gat ggc cag ctg ctg gtg gga gat cct      96
96 Gln Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val Gly Asp Pro
97          20          25          30
99 gtt gca gac aac tgc tgt gca gag aag atc tgc aca ctt cct aac aga      144
100 Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Thr Leu Pro Asn Arg
101          35          40          45
103 ggc ttg gac cgc acc aag gtc ccc att ttc ctg ggg atc cag gga ggg      192
104 Gly Leu Asp Arg Thr Lys Val Pro Ile Phe Leu Gly Ile Gln Gly Gly
105          50          55          60
107 agc cgc tgc ctg gca tgt gtg gag aca gaa gag ggg cct tcc cta cag      240
108 Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro Ser Leu Gln
109 65          70          75          80
111 ctg gag gat gtg aac att gag gaa ctg tac aaa ggt ggt gaa gag gcc      288
112 Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly Glu Glu Ala
113          85          90          95
115 aca cgc ttc acc ttc ttc cag agc agc tca ggc tcc gcc ttc agg ctt      336
116 Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala Phe Arg Leu
117          100          105          110
119 gag gcc gct gcc tgg cct ggc tgg ttc ctg tgt ggc ccg gca gag ccc      384
120 Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu Pro
121          115          120          125
123 cag cag cca gta cag ctc act aag gag agt gag ccc tca gcc cgt acc      432
124 Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser Ala Arg Thr
125          130          135          140
127 aag ttt tac ttt gaa cag agc tgg tag      459
128 Lys Phe Tyr Phe Glu Gln Ser Trp
129 145          150
132 <210> SEQ ID NO: 4
133 <211> LENGTH: 152
134 <212> TYPE: PRT
135 <213> ORGANISM: Homo sapiens
137 <400> SEQUENCE: 4
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140 1          5          10          15
143 Gln Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val Gly Asp Pro
144          20          25          30
147 Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Thr Leu Pro Asn Arg

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148          35          40          45
151 Gly Leu Asp Arg Thr Lys Val Pro Ile Phe Leu Gly Ile Gln Gly Gly
152          50          55          60
155 Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro Ser Leu Gln
156 65          70          75          80
159 Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly Glu Glu Ala
160          85          90          95
163 Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala Phe Arg Leu
164          100          105          110
167 Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu Pro
168          115          120          125
171 Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser Ala Arg Thr
172          130          135          140
175 Lys Phe Tyr Phe Glu Gln Ser Trp
176 145          150
179 <210> SEQ ID NO: 5
180 <211> LENGTH: 21
181 <212> TYPE: DNA
182 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: DNA primer
187 <400> SEQUENCE: 5
188 agaagatctg catacttcct a
191 <210> SEQ ID NO: 6
192 <211> LENGTH: 19
193 <212> TYPE: DNA
194 <213> ORGANISM: Artificial Sequence
196 <220> FEATURE:
197 <223> OTHER INFORMATION: DNA primer
199 <400> SEQUENCE: 6
200 tgagcaggat gagcttggt
203 <210> SEQ ID NO: 7
204 <211> LENGTH: 27
205 <212> TYPE: DNA
206 <213> ORGANISM: Artificial Sequence
208 <220> FEATURE:
209 <223> OTHER INFORMATION: DNA primer
211 <400> SEQUENCE: 7
212 ccatacctaatacgaactcact atagggc
215 <210> SEQ ID NO: 8
216 <211> LENGTH: 18
217 <212> TYPE: DNA
218 <213> ORGANISM: Artificial Sequence
220 <220> FEATURE:
221 <223> OTHER INFORMATION: DNA primer
223 <400> SEQUENCE: 8
224 ctccagctgt aggggaagg
227 <210> SEQ ID NO: 9
228 <211> LENGTH: 23

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229 <212> TYPE: DNA
230 <213> ORGANISM: Artificial Sequence
232 <220> FEATURE:
233 <223> OTHER INFORMATION: DNA primer
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236 actcactata gggctcgagc ggc 23
239 <210> SEQ ID NO: 10
240 <211> LENGTH: 20
241 <212> TYPE: DNA
242 <213> ORGANISM: Artificial Sequence
244 <220> FEATURE:
245 <223> OTHER INFORMATION: DNA primer
247 <400> SEQUENCE: 10
248 tcttctgtct ccacacatgc 20
251 <210> SEQ ID NO: 11
252 <211> LENGTH: 20
253 <212> TYPE: DNA
254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
257 <223> OTHER INFORMATION: DNA primer
259 <400> SEQUENCE: 11
260 caaggctaaa acgcagtttc 20
263 <210> SEQ ID NO: 12
264 <211> LENGTH: 20
265 <212> TYPE: DNA
266 <213> ORGANISM: Artificial Sequence
268 <220> FEATURE:
269 <223> OTHER INFORMATION: DNA primer
271 <400> SEQUENCE: 12
272 caggaaacag ctatgaccat 20
275 <210> SEQ ID NO: 13
276 <211> LENGTH: 22
277 <212> TYPE: DNA
278 <213> ORGANISM: Artificial Sequence
280 <220> FEATURE:
281 <223> OTHER INFORMATION: DNA primer
283 <400> SEQUENCE: 13
284 ctatttaggt gacactatag aa 22
287 <210> SEQ ID NO: 14
288 <211> LENGTH: 538
289 <212> TYPE: DNA
290 <213> ORGANISM: Mus musculus
292 <220> FEATURE:
293 <221> NAME/KEY: CDS
294 <222> LOCATION: (29)..(487)
295 <223> OTHER INFORMATION:
298 <400> SEQUENCE: 14
299 tgaagaccag acactcccaa ctgcagga atg tgc tcc ctt ccc atg gca aga 52
300 Met Cys Ser Leu Pro Met Ala Arg

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301                                     1                               5
303 tac tac ata atc aag gat gca cat caa aag gct ttg tac aca cgg aat      100
304 Tyr Tyr Ile Ile Lys Asp Ala His Gln Lys Ala Leu Tyr Thr Arg Asn
305      10                               15                               20
307 ggc cag ctc ctg ctg gga gac cct gat tca gac aat tat agt cca gag      148
308 Gly Gln Leu Leu Leu Gly Asp Pro Asp Ser Asp Asn Tyr Ser Pro Glu
309 25                               30                               35                               40
311 aag gtc tgt atc ctt cct aac cga ggc cta gac cgc tcc aag gtc ccc      196
312 Lys Val Cys Ile Leu Pro Asn Arg Gly Leu Asp Arg Ser Lys Val Pro
313      45                               50                               55
315 atc ttc ctg ggg atg cag gga gga agt tgc tgc ctg gcg tgt gta aag      244
316 Ile Phe Leu Gly Met Gln Gly Gly Ser Cys Cys Leu Ala Cys Val Lys
317      60                               65                               70
319 aca aga gag gga cct ctc ctg cag ctg gag gat gtg aac atc gag gac      292
320 Thr Arg Glu Gly Pro Leu Leu Gln Leu Glu Asp Val Asn Ile Glu Asp
321      75                               80                               85
323 cta tac aag gga ggt gaa caa acc acc cgt ttc acc ttt ttc cag aga      340
324 Leu Tyr Lys Gly Gly Glu Gln Thr Thr Arg Phe Thr Phe Phe Gln Arg
325      90                               95                               100
327 agc ttg gga tct gcc ttc agg ctt gag gct gct gcc tgc cct ggc tgg      388
328 Ser Leu Gly Ser Ala Phe Arg Leu Glu Ala Ala Ala Cys Pro Gly Trp
329 105                               110                               115                               120
331 ttt ctc tgt ggc cca gct gag ccc cag cag cca gtg cag ctc acc aaa      436
332 Phe Leu Cys Gly Pro Ala Glu Pro Gln Gln Pro Val Gln Leu Thr Lys
333      125                               130                               135
335 gag agt gaa ccc tcc acc cat act gaa ttc tac ttt gag atg agt cgg      484
336 Glu Ser Glu Pro Ser Thr His Thr Glu Phe Tyr Phe Glu Met Ser Arg
337      140                               145                               150
339 taa ggagacataa ggctggggcc tcgtctagtgc cccccagtct gagatcttct t      538
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343 <211> LENGTH: 152
344 <212> TYPE: PRT
345 <213> ORGANISM: Mus musculus
347 <400> SEQUENCE: 15
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353 Gln Lys Ala Leu Tyr Thr Arg Asn Gly Gln Leu Leu Leu Gly Asp Pro
354      20                               25                               30
357 Asp Ser Asp Asn Tyr Ser Pro Glu Lys Val Cys Ile Leu Pro Asn Arg
358      35                               40                               45
361 Gly Leu Asp Arg Ser Lys Val Pro Ile Phe Leu Gly Met Gln Gly Gly
362      50                               55                               60
365 Ser Cys Cys Leu Ala Cys Val Lys Thr Arg Glu Gly Pro Leu Leu Gln
366 65                               70                               75                               80
369 Leu Glu Asp Val Asn Ile Glu Asp Leu Tyr Lys Gly Gly Glu Gln Thr
370      85                               90                               95
373 Thr Arg Phe Thr Phe Phe Gln Arg Ser Leu Gly Ser Ala Phe Arg Leu
374      100                               105                               110
377 Glu Ala Ala Ala Cys Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu Pro

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VERIFICATION SUMMARY

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Input Set : A:\2976-C SeqListce filed 101801.txt

Output Set: N:\CRF3\08122002\J046060A.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date